

1632

Page 1 of 7

412

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/675,509

DATE: 01/23/2002

TIME: 11:18:51

Input Set : A:\73442301.app

Output Set: N:\CRF3\01232002\I675509.raw

ENTERED

3 <110> APPLICANT: FULTON, CHANDLER  
4 LAI, ELAINE Y.  
6 <120> TITLE OF INVENTION: THIAMINASES AND THIAMINASE GENES FOR USE IN APOPTOTIC  
7 THERAPIES  
9 <130> FILE REFERENCE: 073442-0301  
11 <140> CURRENT APPLICATION NUMBER: 09/675,509  
12 <141> CURRENT FILING DATE: 2000-09-29  
14 <150> PRIOR APPLICATION NUMBER: 60/052,377  
15 <151> PRIOR FILING DATE: 1997-07-11  
17 <150> PRIOR APPLICATION NUMBER: 60/087,526  
18 <151> PRIOR FILING DATE: 1998-06-01  
20 <150> PRIOR APPLICATION NUMBER: 60/156,952  
21 <151> PRIOR FILING DATE: 1999-09-29  
23 <160> NUMBER OF SEQ ID NOS: 23  
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35 tccggatata atatcgaata taccgaattt gattgttaca gtgatgctag tcttcaaagt 180  
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39 tttttattgt cctcaccaaa tgggtactcaa caagcatctt ccctttttaga attgggtcaa 420  
40 aagggttggt atgaacaaat tgtttatcca gatgttgcoo cttctagttc tttcacagtt 480  
41 ttccgattgt atcaacaatt actccaatca tcatcatcag ctgcagttga tatcaaggcc 540  
42 tctgatcttc cacaatctgg tgaccaagtc aacaaggata tcaactcaaaa atatagaacc 600  
43 attttggatt caacagttgt tgcctctcaa agagaatata ttaactctgt aaagcaaggt 660  
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87 &lt;210&gt; SEQ ID NO: 2

88 &lt;211&gt; LENGTH: 1025

89 &lt;212&gt; TYPE: PRT

90 &lt;213&gt; ORGANISM: Naegleria gruberi

92 &lt;400&gt; SEQUENCE: 2

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96 Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile
97 20 25 30
99 Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
100 35 40 45
102 Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
103 50 55 60
105 Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
106 65 70 75 80
108 Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
109 85 90 95
111 His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
112 100 105 110
114 Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly

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115	115	120	125
117 Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr			
118 130	135	140	
120 Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Ser Phe Thr Val			
121 145	150	155	160
123 Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ser Ala Ala Val			
124 165	170	175	
126 Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys			
127 180	185	190	
129 Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala			
130 195	200	205	
132 Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser			
133 210	215	220	
135 Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile			
136 225	230	235	240
138 Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys			
139 245	250	255	
141 Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp			
142 260	265	270	
144 Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn			
145 275	280	285	
147 Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn			
148 290	295	300	
150 Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln			
151 305	310	315	320
153 Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg			
154 325	330	335	
156 Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu			
157 340	345	350	
159 Arg Pro Phe Leu Gln His Ile Ala Val Ala Thr Leu Arg Cys Leu Thr			
160 355	360	365	
162 Ala Asp Thr Val Glu Lys Ala Lys Ser Gly His Pro Gly Met Pro Ile			
163 370	375	380	
165 Gly Met Ser Pro Ile Ala Tyr Val Leu Trp Lys Phe Phe Phe Lys Ser			
166 385	390	395	400
168 Ser Lys Asp Asp Val Asn Trp Leu Asn Arg Asp Arg Phe Val Leu Ser			
169 405	410	415	
171 Asn Gly His Gly Cys Thr Leu Leu Tyr Ala Met Leu His Leu Thr Asp			
172 420	425	430	
174 Cys Asn Leu Ser Leu Asp Asp Leu Lys Asn Phe Arg Ser Leu His Ser			
175 435	440	445	
177 Lys Thr Pro Gly His Pro Glu Tyr Gly His Thr Glu Gly Val Asp Ala			
178 450	455	460	
180 Thr Thr Gly Pro Leu Gly Gln Gly Val Cys Asn Ala Ile Gly Met Ala			
181 465	470	475	480
183 Leu Ser Glu Ala His Leu Ala Ala Arg Phe Asn Lys Asp Gly Gln Asn			
184 485	490	495	
186 Ile Phe Asp His His Thr Tyr Val Phe Leu Gly Asp Gly Cys Leu Met			
187 500	505	510	

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189 Glu Arg Val Ala Met Glu Gly Leu Ser Phe Ala Gly His Gln Lys Leu
190      515      520      525
192 Asn Lys Leu Ile Val Phe Tyr Asp Asp Asn Ser Ile Thr Ile Asp Gly
193      530      535      540
195 Lys Thr Glu Leu Thr Phe Thr Gln Asn Thr Pro Glu Val Met Arg Gly
196 545      550      555      560
198 Phe Gly Trp His Val Ile Val Val Asp Lys Ala Asp Asn Asp Leu Val
199      565      570      575
201 Gly Ile Lys Glu Ala Ile Leu Glu Ala His Thr Val Thr Asp Lys Pro
202      580      585      590
204 Ile Met Ile Val Cys Lys Thr Thr Ile Gly Tyr Ser Ser Lys Val Gln
205      595      600      605
207 Gly Thr Ala Lys Val His Gly Ser Pro Leu Gly Ala Asp Gly Leu Lys
208      610      615      620
210 Asn Leu Lys Glu Thr Cys Gly Phe Thr Gly Asn Asp Phe Phe His Val
211 625      630      635      640
213 Pro Glu Ile Val Arg Lys Asp Phe Ala Thr Val Ile Asn Arg Asn Ser
214      645      650      655
216 Glu Lys Leu Ser Gln Trp Lys Gln Val Lys Ser Ala Tyr Asp Thr Thr
217      660      665      670
219 His Ala Thr Glu Ser Gln Leu Leu Gln Arg Met Ile Asn His Glu Leu
220      675      680      685
222 Glu Gly Asp Val Met Glu Lys Leu Pro Lys Tyr Leu Glu Gln Lys Lys
223      690      695      700
225 Ile Ala Thr Arg Ser Thr Ser Gln Gln Val Leu Asn Ala Ile Tyr Pro
226 705      710      715      720
228 Leu Ile Pro Ser Leu Val Gly Gly Ser Ala Asp Leu Thr Pro Ser Asn
229      725      730      735
231 Leu Thr Asp Val Thr Gly Cys Gln Asp Phe Gln Pro Asn Asn Arg Val
232      740      745      750
234 Gly Arg Tyr Ile Arg Phe Gly Val Arg Glu His Ala Met Val Ala Ile
235      755      760      765
237 Ala Asn Gly Ile Leu Tyr His Gly Val Leu Arg Thr Tyr Val Gly Thr
238      770      775      780
240 Phe Leu Asn Phe Ala Ser Tyr Ala Leu Gly Ala Ile Arg Leu Ser Ala
241 785      790      795      800
243 Leu Ser Gly Leu Pro Asn Ile Tyr Val Phe Thr His Asp Ser Ile Gly
244      805      810      815
246 Leu Gly Gln Asp Gly Pro Thr His Gln Pro Val Glu Val Leu Pro Met
247      820      825      830
249 Leu Ile Ala Ile Pro Asn His Ile Val Phe Arg Pro Ala Asp Gly Arg
250      835      840      845
252 Glu Thr Ser Gly Ala Tyr Leu Trp Ala Val Gln Ser Lys Lys Thr Pro
253      850      855      860
255 Ser Ser Met Ile Leu Ser Arg Gln Asp Leu Pro Gln Leu Thr Gly Thr
256 865      870      875      880
258 Asp Ile Ser Lys Val Ala Leu Gly Ala Tyr Val Ile Gln Gly Asp Ala
259      885      890      895
261 Thr Pro Asp Val Val Leu Val Gly Thr Gly Ser Glu Val Ser Leu Met

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264 Val Glu Ala Ala Glu Lys Leu Lys Ala Asn Leu Lys Val Asn Val Val
265          915          920          925
267 Ser Met Pro Ser Trp Glu Leu Phe Val Arg Gln Ser Glu Glu Tyr Arg
268          930          935          940
270 Lys Thr Val Phe Pro Asp Gly Ile Pro Val Val Ser Ala Glu Ala Ser
271 945          950          955          960
273 Ser Thr Phe Gly Trp Thr Ser Phe Ala His Tyr Ala Val Gly Met Thr
274          965          970          975
276 Thr Phe Gly Ala Ser Ala Ala Ala Glu Glu Val Tyr Lys Leu Leu Lys
277          980          985          990
279 Ile Thr Ser Asp Asn Val Ala Glu Lys Ala Thr Lys Leu Val Thr Lys
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285 Leu
286 1025
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292 <213> ORGANISM: Naegleria gruberi
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296 <222> LOCATION: (1)..(1068)
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303 cct tct tgg aat gaa aat ggc aac gaa gtt aaa ttg atc aat ttg atc 96
304 Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile
305 20 25 30
307 aag gat gtt ttg cca act cag gtt tcc gga tat aat atc gaa tat acc 144
308 Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
309 35 40 45
311 gaa ttt gat tgt tac agt gat gct agt ctt caa agt ctt cca gat gtt 192
312 Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
313 50 55 60
315 ttc tca act gat agc att ttc ctt cca tat ctt gtt tct ttg ggt ggt 240
316 Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
317 65 70 75 80
319 gtc aag agt ttg gat gaa tca ttg gtt cgt ggt gtt act ggt gat ttg 288
320 Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
321 85 90 95
323 cat agt ttt gtt tcc tca agt gcc tct gtc aat ggt tcc gtt tat ggt 336
324 His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
325 100 105 110
327 ttc cca caa tac ttg tgc tca aac ttt tta ttg tcc tca cca aat ggt 384
328 Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly
329 115 120 125

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